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Gene expression profile of the herbivore-induced stress responses in *Quercus robur*

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The pedunculate oak (*Quercus robur*) shows high potential for adaption and is therefore a prime candidate to become a pillar of resilient forests in the future to combat the challenges of climate change. The project “Survivor-Oaks” aims to identify oak trees that have increased tolerance to different biotic and abiotic stresses including herbivory, mildew infestation and drought. Tolerant trees will be selected for the establishing future climate seed orchards. Here, we characterize oak trees based on their expression profiles with respect to herbivory. The goal of this study is to compare the expression-level response of oak trees to infestation by two different insects: a specialist, the green oak leaf roller, *Tortrix viridana*, and a generalist, the gypsy moth, *Lymantria dispar*.

In earlier projects, oaks tolerant or susceptible to *T. viridana* have been identified based on defoliation rates in several high-infestation years. We conducted two separate feeding experiments with the two above mentioned insects using three tolerant and three susceptible oak clones. High-throughput RNA-seq data have been generated and analysed by mapping the data versus a new chromosome-level reference genome of *Q. robur* and differential gene expression analysis with Deseq2. Functional studies were performed using Gene Ontology over-representation and enrichment analyses of genes expressed differentially in response to the two herbivores. The stress responses revealed as well similarities but also differences in the reaction of *Q. robur* to *T. viridana* and *L. dispar*. (e.g., an enrichment of terpene synthase-related terms or regulation of the jasmonate pathway).

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Saltational evolution: a case study in *Capsella bursa-pastoris*

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Over the last two decades, the *Stamenoid petals* (*Spe*) variants of shepherd’s purse (*Capsella bursa-pastoris*) have been developed into a model system for studying saltational evolution [1, 2]. *Spe* plants represent homeotic mutants in which the petals are transformed into functional stamens, whereas all other organs of the flower are as in the wildtype. The ecophysiological mechanisms that enable *Spe* plants to co-exist in sympatry with wild-type plants in natural populations over decades are relatively well understood [3-7]. The molecular mechanism that generated *Spe* plants in the first place remain elusive, however. We used comparative sequence analysis, classical gene mapping approaches, gene expression studies and genome editing by CRISPR-Cas9 to elucidate the underlying mutation. Here we report that one *Spe* variant was generated by a 6.8 kb insertion of a non-LTR retrotransposon 2 kb upstream of the coding region of one of the two *AGAMOUS*-loci (*CbpAGa*) of *Capsella bursa-pastoris*. This generated a semi-dominant mutant allele (*CpbAGa-Spe*) that is ectopically expressed in the second floral whorl. Since *AGAMOUS* genes provide the floral homeotic C function involved in specifying stamens [8], this finding readily explains the homeotic transformation of second whorl organs into stamens in *Spe* plants, as previously hypothesized [1, 2]. Our results support the view that a radically deviant variant, that has historically even been considered as a new species (*Capsella apetala*), can occur by a simple genetic change within one generation which is the hallmark of saltational evolution.

References

1. Nutt, P., et al. (2006) *Pl. Syst. Evol.* **259**, 217-235
2. Hintz, M., et al. (2006) *J. Exp. Bot.* **57**, 3531-3542
3. Ziermann, J., et al. (2009) *Planta* **230**, 1239-1249
4. Hameister et al. (2009) *Mol. Ecol.* **18**, 2659-2667
5. Hameister, S., et al. (2013) *Flora* **208**, 641-647
6. Hameister and Neuffer (2017) *Plant Ecol. Evol.* **150**, 67-75
7. Neuffer et al. (2020) *PeerJ* **8**:e9226
8. Theißen, G., et al. (2016) *Development* **143**, 3259-3271